AW619116 436 MARC AA785019 uj22e09.x AA653070 nc49b06.s AA659567 nc49b06.s AA215085 uj23904;xv; AA217085 rPCI-23-2 AA22714 nc49b06.r AZ267276 RPCI-23-1 B1837100 ZF637-1-0 AI659563 tu12d12.x AW619096 424 MARC B1979490 ft88b09.y AL706143 DKFZp6866. B118333 UNL-P-FN-

T28396 EST41738 Hu

A1326670 mo60g04.y A1893550 mo60g04.x A1317523 uj23g04.y BQ049864 AGENCOURT AMC19117 437 MARC AA089319 mo60g04.r AU136010 AU136010

BM714196 UI-E-EJO-BM714773 UI-E-EJO-BM714773 UI-E-EJO-BG945621 dd89410: Y FG886115 dad73b08: Y FG886115 dad73b08: Y FG886115 dad73b08: Y FG86115 ultiple: W FG97346 WR4-HT105 BB666485 BB666485 AU139958

BG614664 602642157 AW910225 ur79c10.y AZ303301 UP_479-1J AA252234 zr63h08.r

Result No.

OM nucleic

Run on:

Sequence:

Minimum DB Maximum DB

Database

Searched:

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AW951855 654 bp mRNA linear EST 01-JUN-2000 EST363925 MAGE resequences, MAGB Homo sapiens cDNA, mRNA sequence.
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Hegde, P., Qi.R., Abernathy, K., Dharap, S., Gaspard, R., Gay, C., Holt, J.E., Saeed, A.I., Sharov, V., Lee, N.H., Yeatman, T.J. and Quackenbush, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Assessment of gene expression patterns in a model of colon tumor interatesis using a 19,200 element cDNA microarray Unpublished (2000) Contact: John Quackenbush Contact: John Quackenbush The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD 20850, USA Tel: 301 838 3528 Fax: 301 838 0208 Fax: Johnq@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Seq primer: Reverse.
Location/Qualifiers
1. .654
/organism="Homo sapiens"
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AW619096
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BB612466 BB612466
AA524966 MB55cll.s
AI317423 uj22e09.y
AA229063 nc49907.s
                                                                               8, 2003, 14:51:24 ; Search time 6124 Seconds (without alignments) 13439.821 Million cell updates/sec
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                                                                                                                                                               Description
                                                                                                                                                                                                                                                                   32308132
     GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                         Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                   16154066 seqs, 8097743376 residues
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                                                         nucleic search, using sw model
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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em_gss_pro:*
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em_gss_hum:*
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bunnalla; Eutherla; Primates; Catarrhini; Hominidae; Homo.
(Dases 1 to 532)
Poustka,A., Wellenreuther,R., Mewes,H.W., Well,B. and Wiemann,S.).
ST, (Poustka,A., Wellenreuther,R., Mewes,H.W., Well,B. and Wiemann,S.).
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                                                                                               27; Indels
           MAGB"
                                                                       DB 10;
                                                                     Score 571.8; DB 1
Pred. No. 1.2e-71;
0; Mismatches 27
       /clone_lib="MAGE resequences,
/note="Vector: pBluescriptSKm"
183 c 133 g 172 t
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DKFZp686A1931 5', mRNA sequence.
AL704463
/db_xref="taxon:9606"
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                                                                    11.3%;
95.3%;
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Unpublished (1999)
Contact: Poustka A.J.
                                                                                               Matches 622; Conservative
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AUTHORS
TITLE
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3694 CGAAGGAAAATTGTCCATCTTGTCGTCTTCGGAAATGTTATGAAGCAGGGATGACTCTG 3753
Department Lehrach
Max-Planck-Institute for Molecular Genetics
Innestrasse 73 14195 Berlin, Germany
Tel: +49-30-84131623
Fax: +49-30-84131128
Email: poustka@mpimg-berlin-dahlem.mpg.de
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKF2); Email s.wiemann@dkfz- heidelberg.de;
sequenced by DKFZ (German Cancer Research Center,
Heidelberg/Germany) within the CDNA sequencing consortium of the
German Genome Project.
No sl sequence available.
This clone (DKFZp686A1931) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
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6, 14059
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cDNA-collection"
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Pred. No. 1.5e-65;
----nes 3; Indels
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                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="DkFzp686A1931"
/clone_lib="686 (synonym: hlcc3)"
/tissue_type="human skeletal muscle"
/dev_stage="adult"
/lab_host="DH108"
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Best Local Similarity 99.4%;
Matches 529; Conservative
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(Mono, H., Fukunishi, Y., Shibata, K., Itch, M., Carninci, P., Sugahara Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) Yamanaka, L., Klosawa, H., Kondo, S., Saito, T., Shinagawa, A., Aizawa Ishii, Y. and Hayashizaki, Y. (Somome Res. 11 (2), Shinagawa, A., Aizawa Ishii, Y. and Hayashizaki, Y. (Somome Somomics 2), Struct. Func. Genomics 2 pre, L72-L86 (2001) Please visit our web site (http://genome.gsc.riken.go.jp) for
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Arakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., H.; Moya, S., Matsuyama, T., Myazaki, A., Nomura, K., Ohno, H., Kouda, Okazaki, Y., Okido, T., Saito, F., Sataki, R., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Soqabe, Y., Suzuki, H., Muramatsu, M., and Hayashizaki, Y.

Firgami, M., and Hayashizaki, Y.

Gupublished (2001)
BB612466 BIKEN full-length enriched, O day neonate skin Mus
musculus cDNA clone 4632412C07 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: genome-reseggs.riken.go.jp,
URL:http://genome.go.go.
URL:http://genome.go.go.
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
Prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1517-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Matahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
Hayashizaki,Y.
nokazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute The Institute of Physical and Chemical Research (RIKEN) 1-7-22 Suchiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Fax: 81-45-503-9216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="Site_1: Sal1; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone_lib="RIKEN full-length enriched, 0 day neonate
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/dev_stage="0 day neonate"
/lab_host="DH10B"
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/clone="4632412C07"
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COMMENT

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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                                                                                                                                                                                                                       3642 GAAACAGAAGTACCTGTGCGCCAGCAGAAATGATTGCACTATTGATAAATTCCGAAGGAA 3701
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                                                                                                                                                                                                     ;
                                                                                                                                                                       Score 519.4; DB 10; Length 634;
Pred. No. 3.1e-64;
0; Mismatches 71; Indels 0;
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                                                                                                          Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Email: gapbs-rémail.nih.gov
Tissue Procurement: W. Marston Linehan, M.D., Rodrigo Chuaqui, M.D.
Tissue Procurement: W. Marston Linehan, M.D., Rodrigo Chuaqui, M.D.
Nichael Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: David B. Krizman, Ph.D.
CDNA Library Parayed by: Genome Systems Inc., Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-GAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LINL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 362 Std Error: 0.00
Seq primer: -40ml3 fwd. Erf from Amersham
High quality sequence stop: 383.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /Acce_wost__nature
//Acctor: pAMP10; Site_1: Not1; Site_2: ECORI; 1st
strand CDNA was prined with Oligo(dT)17 on 50 ng of
BUNSe-treated, total cellular RNA obtained from 5,000-10
000 microdissected cells histologically-determined to be
fully malignant prostate cancer cells. Double-stranded
CDNA was ligated to EcoRI adaptors, 5 cycles of PCR
applied to the CDNA with an adaptor-specific primer, and
the resulting PCR product subcloned into pAMP10 by the
UDG-cloning method (Life Technologies). Average insert
size is 600 bp. NOTE: Not directionally cloned. This
library was constructed by David Krizman."

16 a 99 c 153 g 130 t
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                      1 (bases 1 to 568)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    191 ATCTGTGTTTTGAATGGTGTTGTATGCCTTTAAATCTGTGATGATCGTCGTATTGGCCCAG 132
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Pred. No. 1.2e-61;
0; Mismatches 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone_lib="NCI_CGAP_Pr3"
/sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /dev_stage="45 years old"
/lab_host="DH10B"
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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Conservative (
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Size selection was
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                                                                                                                                                                                EST 17-DEC-1998
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 724)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            free through LLNL; contact the nl.gov) for further information.
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A1317423 724 bp mRNA linear EST 17-DEK uj22e09.yl Sugano mouse kidney mkia Mus musculus cDNA clone IMAGE:1920712 5' similar to gb:X53779 Mouse mRNA for androgen receptor (MOUSE);, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The WashU-HHMI Mouse EST Project
Unpublished (1996)
Contact: Marra MyMouse EST Project
WashU-HHMI Mouse EST Project
WashIngton University School of MedicineP
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Fax: 314 286 1800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 724;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone="IMAGE:1920712"
/clone_lib="Sugano mouse kidney mkla"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This clone is available royalty-free throug IMAGE Consortium (info@image.llnl.gov) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 462.2; DB 9;
Pred. No. 3.6e-56;
0; Mismatches 113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1. .724
/organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: mouseest@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Seq primer: custom primer used
High quality sequence stop: 515.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /strain-"C57BL"
/db_xref-"taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /dev_stage="adult"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /sex="female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9.1%;
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AI317423.1 GI:4032690
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Best Local Similarity 82.8
Matches 564; Conservative
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RESULT 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Issue Procurement: W. Marston Linehan, M.D., Rodrigo Chuaqui, M.D.
Michael Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: David B. Krizman, Ph.D.
CDNA Library Arrayed by: Genome Systems Inc., Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
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NCI-GGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Unpublished (1997)
                                                 GCTACACTCGGCCCCCTCAGGGGCTGGCGGGCCAGGAAAGCGACTTCACCGCACCTGATG 3376
                                                                                                           3436
                                                                                                                                                                                                    CIGCCAGGGACCAIGITITGCCCAITGACIATTACITITCCACCCAGAAGACCIGCCTGA 3556
                                                                                                                                                                                                                                                     TCTGTGGAGATGAAGCTTCTGGGTGTCACTATGGAGCTCTCACATGTGGAAGCTGCAAGG 3616
                                                                                                                                                                                                                                                                                                      TCTTCTTCAAAAGAGCGGCTGAAGGGAAACAGAAGTACCTGTGCGCCCAGCAGAAATGATT 3676
                                                                                                                                                                                                                                                                                                                                                        GCACTATTGATAAATTCCGAAGGAAAATTGTCCATCTTGTCGTCTTCGGAAATGTTATG 3736
                                                                                                                                                             3496
                                                                                                                                                                                                                                                                                                                                                                                                         AAGCAGGGATGACTCTGGGAGCCCGGAAGCTGAAAACTTGGTAATCTGAAACTACAGG 3796
                                                                                                                                                                                                                                                                                                                                                                                                                                                           AGGAAGGAGAGGCTTCCAGCACCACCACCACTGAGGAGACAACCCAGAAGCTGACAG 3856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TGTCACACATTGAAGGC-TATGAATGTCAGCCCATCTTT--CTGAATGTCCTGGAAGCCA 3913
                                                                                                                                  194
                                                                                                                                                                                     254
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GCGGCGGCGGCGGCGGCGGCGGCGGCGAGGCGGGAGCTGTAGCCCCTACG
                TGTGGTACCCTGGCGGCATGGTGAGCAGAGTGCCCTATCCCAGTCCCACTTGTGTCAAAA
                                                                                                                GCGAAATGGGCCCCTGGATGGATAGCTACTCCGGACCTTACGGGGACATGCGTTTGGAGA
                                                                                                                                                                  3914 TTGAGCCAGGTGTAGTGTG 3934
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 3257
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TITLE
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AA229063
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//note="Vector: paMp10; Site_1: Not1; Site_2: EcoRI; 1st strand cDNA was primed with oligo(dT)17 on 50 ng of DNAse-treated, total cellular RNA obtained from 5,000-10,000 microdissected cells histologically-determined to be fully malignant prostate cancer cells. Double-stranded cDNA was ligated to EcoRI adaptors, 5 cycles of PCR applied to the cDNA with an adaptor-specific primer, and the resulting PCR product subcloned into pAMP10 by the UDG-cloning method (Life Technologies). Average insert size is 600 bp. NOTE: Not directionally cloned. This library was constructed by David Krizman."
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
            can
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CAGAGATCATCTGTGCAAGTGCCCAAGATCCTTTCTGGGAAAGTCAAGCCCATCTATT 4621
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4622 TCCACACCCAGTGAAGCATTGGAAACCCTATTTCCCCACCCCAGCTCATGCCCCCTTTCA 4681
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GATGTCTTCTGCCTGTTATAACTCTGCACTACTCCTCTGCAGTGCCTTGGGGAATTTCCT 4741
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AA229062 369 bp mRNA linear EST 21-AUG-nc49907.rl NCI_CGAP_Pr3 Homo sapiens cDNA clone IMAGE:1011516 similar to gb:M23263 ANDROGEN RECEPTOR (HUMAN);, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61
  Clone distribution: NCI-CGAP clone distribution information found through the I.M.A.G.E. Consortium/LINL at:
www.blo.llnl.gov/bbrp/image.html
Seq primer: -41ml3 fwd. ET from Amersham
High quality sequence stop: 366.
Location/Qualifiers
1. 388
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .7e-44;
                                                                                                                                       /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="InAGE:1011516"
/clone_lib="NCI_CGAP_Pr3"
/sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 380.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. 1.7e
0; Mismatches
                                                                                                                                                                                                                                              /dev_stage="45 years old"
/lab_host="DH10B"
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AA229062.1
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Clone
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source
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JOURNAL
COMMENT
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RESULT 8
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                                                                                                                                                                      ACCESSION
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                                                                                                                                                                                                                                      KEYWORDS
                                                                                                                                                                                                                                                                  SOURCE
                                                                                                                                                        Contact: Robert Strausberg, Ph.D.
Email: cgapbs.remail.nih.gov
Tissue Procurement: W. Marston Linehan, M.D., Rodrigo Chuaqui, M.D.
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Tissue Procurement: W. Marston Linehan, Ph.D.
CDNA Library Preparation: David B. Krizman, Ph.D.
CDNA Library Arrayed by: Genome Systems Inc., Greg Lennon, Ph.D.
DNA Sequencing by: Mashington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.lln!gov/bbpy/image/image.html
Seq primer: -28ml3 revl ET from Amersham
High quality sequence stop: 341.
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//dev_stage="45 years old"
//dev_stage="1000"
//dev_stage="1000
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                                              NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4680 CAGATGTCTTCTGCCTGTTATAACTCTGCACTACTCCTCTGCAGTGCCTTGGGGAATTTC 4739
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/organism="Homo sapiens"
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1011516"
/clone_lib="NCI_CGAP_PF3"
/sex="Male"
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                                                                                                                 Tumor Gene Index
Unpublished (1997)
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Unpublished (2001)
Contact: Yoshinide Hayashizaki
Sciences Center(GSC), Yoshama Institute
Sciences Center(GSC), Yoshama Institute
The Institute of Physical and Chemical Research (RIKEN)
The Institute of Physical and Chemical Research (RIKEN)
The Institute of Physical and Chemical Research (RIKEN)
The Institute of Physical and Chemical
Fax: 81-45-503-922
Fax: 81-45-503-922
Fax: 81-45-503-9216
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                                                                                                                                                                                                                                                                                                                                                                                                                         Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; ¡Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases I to 628)
Arakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A.,
Hiramoto, K., Hori, F., Ishii, Y., Ito, M., Kawai, T., Kohno, H., Kouda
, M., Koya, S., Mateyama, T., Miyazaki, A., Nomura, K., Ohno, M.,
Ckazaki, Y., Okido, T., Sakio, R., Sakai, C., Sakai, K., Sano, H., Sasaki
, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H.,
Tagami, M., Tagawa, A., Takahashi, F., Takeda, Y., Tanaka, T., Toya, T.,
RIKEN Mouse ESTS (Arakawa, T., et al. 2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000) Konno, H., Evkunishi, Y., Shibata, R., Itoh, M., Carninci, P., Sugahara K., Itoh, M., Carninci, P., Sugahara
628 bp mRNA linear: EST 26-OCT-2001 RIKEN full-length enriched, adult male pituitary gland Mus cDNA clone 5330428G13 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /nore==Site_1: Sall; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Computational Analysis of Full-Length Mouse cDNAs Compared will Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001) Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone="5330428G13"
/clone_1b="RIKEN full-length enriched, adult male
pituteary gland"
/sex="male"
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/dev_stage="adult"
/lab_host="DH10B"
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/db_xref="taxon:10090"
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us-09-497-822c-18.rst

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1864 ATGGAAGTGCAGTTAGGGCTGGGAAGGGTCTACCCTCGGCCGCCGTCCAAGACCTACCGA 1923
                                                                                                                                                                                                    1924 GGAGCTITCCAGAATCTGTTCCAGAGCGTGCGCGAAGTGATCCAGAACCCGGGCCCCAGG 1983
                                                                                                                                          1804 GAGCAAGAGAGGGGAGGCGGGTAAGGGAAGTAGGTGGAAGATTCAGCCAAGCTCAAGG 1863
                                                                                                                                                                                                                                  2104 CAGCAAGAGACTAGCCCCAGGCAGCAGCAGCAGCAGGAGGGTGAGGATGGTTCTCCCCAA 2163
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                                                                                                                                                                                                                                                                                                     413
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                                                                                                                                                                                                                                                                                                                                                                -----ACAGCAGAGG
                                                                                                              Score 368.4; DB 10; Length 628;
Pred. No. 7.1e-43;
0; Mismatches 91; Indels 69:
                                                                                                                                91; Indels
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                                                                                                                      Local Similarity
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linear EST 06-SEP-1995 end similar to androgen

T28396 413 bp mRNA EST41738 Human Uterus Homo sapiens cDNA 5' receptor (HT:1334), mRNA sequence.

LOCUS

RESULT 9 T28396

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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhin!; Hominidae; Homo.

1 (Dases) 1 to 413)

2 (Dases) 1 to 413)

2 (Adams, D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A., Bult C.J., Lee, N., Kirkness, E.F., Weinstock, K.G., Googyne, J.D., White C.J., Lee, N., Fitzkerald, J., Fine, L.D., Fitzgerald, L.M., Fitzklugh, W.M., Fitzkerald, J., Fine, L.D., Kelley, J.M., Kirkman, J.C., Geoghagen, N.S.M., Glodek, A., Kilmek, K.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M., Moreno-Palanques, R.F., McDonald, L.A., Nguyen, D.T., Pelley, J.M., Moreno-Palanques, R.F., McDonald, L.A., Nguyen, D.T., Pelley, J.M., Phillips, C.A., Ryder, S.E., Soott, J.L., Saudek, D.M., Shirley, R.M., Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, R. J., Dimke, D., Ferrich, R., Fischer, C., Hastings, G.A., He, W.-W., Kunsch, C., Jill, H., Meissner, P.S., Olsen, H., Raymond, D., Weiter, J.T., Ming, J., Xu, C., Yu, G.-L., Hudson, P., Kim, A., Kozak, D.L., Willey, J., H., Lill, H., Meissner, P.S., Olsen, H., Raymond, D., Weiter, J.C., Weiter, J.C., The Land, R., Fensen, C., Thillon, P.J., Fannon Venter, J.C., Thillon, P.J., Franco, M.R., Rosen, C.A., Haseltine, W.A., Fields, C., Fraser, C.M., and Venter, J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Initial Assessment of Human Gene Diversity and Expression Patterns
Based Upon 83 Million Basepairs of cDNA Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Database
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: tdbinfo@tdb.tigr.org
For clone availability, additional sequence and expression information related to this EST, please contact:the TIGR De (tdbinfo@tdb.tigr.org)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4167 CGCCCCTGATCTGGTTTTCAATGAGTACCGCATGCACAAGTCCCGGATGTACAGCCAGTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
/db_xref="ATCC (inhost):102309"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The Institute for Genomic Research 932 Clopper Rd, Gaithersburg, MD 20878 Tel: 3018699056 Fax: 3018699423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ų
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/note="Organ: uterus"
108 c 92 g 107
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                         GI:610494
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                                                                                         Homo sapiens
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                                       KEYWORDS
SOURCE
ORGANISM
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VERSION
                                                                                                                                                      REFERENCE
                                                                                                                                                                             AUTHORS
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556 ACAGCA 561
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AUTHORS
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PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4356
Fax: 402 762 4390
Famil: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the minscore 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ä
                                                                                                                                                             EST 24-MAR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="Vector: pBLUBSCRIPT SK-; Site_1: EcoR1; Site_2: Xho1; Library made from pool of embryos in spherical and filamentous stages of development (7.5% and 92.5%, respectively, of each stage) as described in Choi et al, redocrinology 137, 1457-67, 1996."
                                                                                                                                                                                                                                                               Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

1 (bases 1 to 573)

Smith, T.P.L., Fahrenkrug, S.C., Rohrer, G.A., Simmen, F.A., Rexroad, C.E. and Keele, J.W.

Mapping of expressed sequence tags from a porcine early embryonic cDNA library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1983 GCACCCAGAGGCCGCGAGCGCAGCACCTCCCGGCGCCAGTTTGCTGCTGCTGCTGCAGCAGCA 2042
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1863 GATGGAAGTGCAGTTAGGGCTGGGAAGGGTCTACCCTCGGCCGCCGTCCAAGACCTACCG 1922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       130 ACACCCTGAGGCCGCAGCGCAGCACCTCCCGGCGCCGTTTGCAGCAGCAGCAGCTGCA 189
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Gaps
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                                                                                                                                                                AW619116 573 bp mRNA line:
436 MARC PBE Sus scrofa cDNA 5', mRNA sequence.
AW619116 1 GI:7325300
                                                            CAAAAGAAAAATCCCACATCCTGCTCAAGACGCTTCTACCAG 4449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /tissue_type="Day 12 whole embryos"
/lab_host="XLOLR"
                                                                          CAAAAGGAAAAATCCCACATCTGNTTCAGACGGTTTTACCAG 402
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tch 7.1%; Score 358.4; DB al Similarity 77.7%; Pred. No. 2e-41; 471; Conservative 0; Mismatches 8
                                                                                                                                                                                                                                                                                                                                                                Anim. Genet. 32 (2), 66-72 (2001)
21314990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FORWARD: GGAAACAGCTATGACCATG
BACKWARD: GTAAAACGACGGCCAGT
Seq primer: AATTAACCCTCACTAAAGGG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Sus scrofa"
/db_xref="taxon:9823"
/clone_lib="MARC PBE"
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1. .573
                                                                                                                                                                                                                                            pig.
Sus scrofa
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Matches 471
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linear . EST 02-JUL-1999
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Eukaryota, Metazoa; Chordata; Craniata; Vertebráta; Suteleostomi;
Mamalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 637)
Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T.,
Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T.,
Bonderwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R.,
The Washu-NCI Mouse EST Project 1999
Unpublished (1999)
Other ESTs uj2e909.71
                                                                                                                                                                                                                     This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                 2283 CGTGGCCGCCAGCAAGGGGCTGCCGCAGCAGCTGCCAGCACCTCCGGACGAGGATGACTC 2342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2462
                                                                                                                                                                                                       GCCGCAGTCGCCCTGGAGTGCCACCCCGAGAGAGTTGCGTCCCAGAGCCTGGAGCCGC 2282
                                                                                                                                                                                                                                                                                                                                                                                     AGCCCATCGTAGAGGCCCCCACCAGGCTACCTGGATGAGGAACAGCAACCTTCACA 2222
                                                                                                                                                                                                                                                                                                                        uj22e09.x1 Sugano mouse kidney mkia Mus musculus.cDNA clone IMAGE:1920712 3' similar to gb:X53779 Mouse mRNA for androgen receptor (MOUSE);, mRNA sequence.
A1785019
A1785019. GI:5332735
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Mara M/WashU-NCI Mouse EST Project 1999
Contact: Marra M/WashU-NCI Mouse EST Project 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2403 CGCTGACCTTAAAGACATCCTGAGCGAGGCCAGCACCATGCAACTCCTTCAGCAACAGCA
                                /clone_lib="Sugano mouse kidney mkia"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Mus musculus"
/strain="C57BL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Seq primer: custom primer used
High quality sequence stop: 518.
Location/Qualifiers
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/clone="IMAGE:1920712"
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/dev_stage="adult"
190 GCAGCAGGACCAGTCCCCGGCGGCA--
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/note="Organ: Kidney; Vector: pME185-FL3; Site_1: DraIII (CACCATGTG); Ist strand cDNA Was primed with an oligo(dT) primer (ATGTGGCCTTTTTTTTTTTTTTTT); double-stranded cDNA was ligated to a DraIII adaptor [TGTTGGCCTACTGG], digested and cloned into distinct DraIII sites of the PME185-FL3 vector (5' site CACTGTGG, 3' site CACCATGTG, ENOIS be used to isolate the CDNA insert. Size selection was performed to exclude fragments. C.15kb. Library constructed by Dr. Sumio Sugano (University of Tokyo Institute of Medical Science). Custom primers for sequencing: 5' end primer CTGTGTGTTAAAAGCTGCG and 3' end primer CGACCTGCAGCACCCAACCACTTAAAAGCTGCG and 3' end 11 a 118 c. 168 g 139 t. 1 others
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                                                                                                                                                                                                                                 4420 CCCACATCCTGCTCAAGACGCTTCTACCAGCTCACCAAGCTCCTGGACTCCGTGCAGCCT 4479
                                                                                                                                                                                                                                                                             4480 ATTGCGAGAGAGCTGCATCACTTTTGACCTGCTAATCAAGTCACACATGGTGAGC 4539
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                                                                                                                                                                                                                                                                                                                                                                                                                     ACCCCAGCTCATGCCCCCTTTCAGATGTCTTCTGCCTGT--TATAACTCTGCACTACTCC 4716
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4717 TCTGCAGTGCCTT-GGGGAATTTCCTCTATTGATGTACAGTCTGTCATGAACATGTTCCT 4775
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                                                                                                                                                                                                                 98; Indels
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Pred. No. 2.2e-41;
0; Mismatches 98
                                                                                                                                                                                      Query Match 7.0%;
Best Local Similarity 81.4%;
Matches 529; Conservative
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Best Local (
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AA230070 349 bp mRNA linear EST 21-AUG-1997 nc49b06.s1 NCI_CGAP_PT3 Homo sapiens cDNA clone IMAGE:1011443 similar to gb:M23263 ANDROGEN RECEPTOR (HUMAN);, mRNA sequence.

AA230070.1 GI:1852363

ACCESSION VERSION

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Contact: Robert Strausberg, Ph.D.

Email: cgapbs-rémail.nih.gov
   Tissue Procurement: W. Marston Linehan, M.D., Rodriyo Chuaqui, M.D.
   Tissue Procurement: W. Marston Linehan, M.D., Rodriyo Chuaqui, M.D.
   CDNA Library Preparation: David B. Krizman, Ph.D.
   CDNA Library Prayed by: Genome Systems Inc., Greg Lennon, Ph.D.
   DNA Sequencing by: Washington University Genome Sequencing Center
   Clone distribution: NCI-CGAP clone distribution information can be
   www-bio.llnl.gov/bbrp/image/image/image.html
   Seq primer: -41ml3 fwd. ET from Amersham
   High quality sequence stop: 230.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 / Jobe - Weetor: DAMPIO; Site_1: Not1; Site_2: EcoRI; 1st strand cDNA was primed with oligo(dT)17 on 50 ng of DNASe-treated, total cellular RNA obtained from 5,000-10,000 microdissected cells histologically-determined to be fully malignant prostate cancer cells. Double-stranded cDNA was ligated to EcoRI adaptors, 5 cycles of PCR applied to the cDNA with an adaptor-specific primer, and the resulting PCR product subcloned into pAMPIO by the UDG-cloning method (Life Technologies). Average insert size is 600 bp. NOTE: Not directionally cloned. This library was constructed by David Krizman."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4540 GIGGACITICCGGAAAIGAIGGCAGAGAICAICICIGIGCAAAIGCCCAAGAICCTITCI 4599
                Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 349)

NCI-GAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index

Onpublished (1997)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1. 349 // Crganism="Homo sapiens" // db_aref="taxon:9606" // clone="IMAGE:1011443" // clone_lib="NCI_CGAP_Pr3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /dev_stage="45 years old"
/lab_host="DH10B"
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Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                             Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: W. Marston Linehan, M.D., Rodrigo Chuaqui, M.D.,
Tissue Procurement: W. Marston Linehan, M.D., Rodrigo Chuaqui, M.D.,
Nichael Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: David B. Krizman, Ph.D.
CDNA Library Preparation: David B. Krizman, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NNI-C&PR clone distribution information can be
found through the I.M.A.G.E. Consortium/LINL at:
www-bio.llni.gov/Dbpp/Amage/Amage.html
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 360.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /dev_stage="45 years old"
/dev_stage="45 years old"
/lab_host="NH10B"
/note="vector: pAMPI0; Site_1: Not1; Site_2: EcoRI: 1st
strand cDNA was primed with oligo(d7)17 on 50 ng of
bNAse-treated, total cellular RNA obtained from 5,000-10
,000 microdissected cells histologically-determined to be
fully malignant prostate cancer cells. Double-stranded
cDNA was ligated to EcoRI adaptors, 5 cycles of PCR
applied to the cDNA with an adaptor: specific primer, and
the resulting PCR product subcloned into pAMPI0 by the
UDG-cloning method (Life Technologies). Average insert
size is 600 bp. NOTE: Not directionally cloned. This
library was constructed by David Krizman."
                                   179 bp mRNA linear EST 05-NOV-1997 nt63a03.s1 NCI_CGAP_Pr3 Homo sapiens cDNA clone IMAGE:1203148 similar to gb:M23263 ANDROGEN RECEPTOR (HUMAN);, mRNA sequence. AA659567 AA659567.1 GI:2595721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5;
                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. I Chases 1 to 379; NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4765 AACATGTTCCTGAATTCTATTTGCTGGGCTTTTTTTTTCTCTTTCTCTTTTTC 4824
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1203148"
/clone_lib="NCI_CGAP_Pr3"
/sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 6.8
Best Local Similarity 98.1
Matches 371; Conservative
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Unpublished (1997)
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/note="Organ: Kidney; Vector: pWE18S-FL3; Site_1: DraIII (CACTGTGTG); 1st strand cDNA was primed with an oligo(df) primer and primed with an oligo(df) primer arranged cDNA was ligated to a DraIII adaptor (TGTTGGCCTACTGG) digested into distinct DraIII sites of the pWE18S-FL3 vector (5' site CACTGTGTG, 3' site CACATGTG; XhoI should be used to isolate the cDNA insert. Size selection was performed to exclude fragments <1.5kb. Library man.
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Eukaryota, Matazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 536)
Marra M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
Schellenberg, K., Steptoe, M., Tan, P., Underwood, K., Moore, B.,
Theising, B., Wylle, T., Lennon, G., Soares, B., Wilson, R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       constructed by Dr. Sumio Sugano (University of Tokyo Institute of Medical Science). Custom primers for sequencing: 5' end primer CTTCTGCTCTAAAAGCTGGG and 3' end primer CGACCTGGAGCACA." 1 others
                                                                                                                                                                                                                                                                                                                                                                                                                EST 17-DEC-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the:
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:977114
                                                                                 117-DEC 536 bp mRNA linear EST 17-DEC uj23904.x1 Sugano mouse kidney mkia Mus musculus cDNA clone IMAGE:1920822 3' similar to gb:X53779 Mouse mRNA for androgen receptor (MOUSE);, mRNA sequence.
Waterston, R.
The WashU-HHMI Mouse EST Project
Unpublished (1996)
Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Parkway, Box 8501, St. Louis, MO.63108
Fax: 314 286 1800
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/sex="female"
/dev_stage="adult"
/lab_host="DH10B"
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/strain="C57BL"
/db_xref="taxon:10090"
/clone="IMAGE:1920822"
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Search completed: May
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RPCI-23-259K23.TV RPCI-23 Mus musculus genomic clone RPCI-23-259K23
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Mouse BAC End Sequences from Library RPCI-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 498)
                                               4531 ATGGTGAGCGTGGACTTTCCGGAAATGATGGCAGAGATCATCTCTGTGCAAGTGCCCAAG 4590
                                                                                                    4591 ATCCTTTCTGGGAAAGTCAAGCCCATCTATTTCCACACCCAGTGAAGCATTGGAAACCCT 4650
                                                                                                                                                             ATTTCCCCACCCCAGCTCATGCCCCCTTTCAGATGTCTTCTGCCTGT--TATAACTCTGC 4708
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                                                              ACTACTTCTGCAGTGCCTTGGGGGAAATTCCTCTACTGATGTACAGTCTGTCGTGAAAC 298
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                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: szhao@tigr.org
Clones are derived from the mouse BAC library RPCI-23. For BAC
library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
                                                                                                                       ACTACTCCTCTGCAGTGCCTT-GGGGAATTTCCTCTATTGATGTACAGTCTGTCATGAAC
                                                                                                                                                                                                                                                                                             4888 ATCTGTGTTTTGAATGGTGTTGTATGCCTTTAAATCTGTGATGATCCTCATATGGCCCAG
                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (1993)
Other GSSs: RPCT-23-259K23.TJ
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, 17el: 301 838 0200
         No. 7.6e-36;
smatches 81;
          Pred. No. 7.6e
); Mismatches
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Best Local Similarity 81.7 Matches 446; Conservative
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BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm) or from Resea ch Genetics (info@resgen.com). BAC end page: http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html Plate: 259 row: K column: 23 Sep primer: T7 Class: BAC ends.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2345 CTGCCCCATCCACGTTGTCCCTGCTGGCCCCCACTTTCCCCGGCTTAAGCAGCTGCTCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5.8%; Score 293.2; DB 17; Length 498; 73.9%; Pred. No. 3.5e-32; Live 0; Mismatches 79; Indels 69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     1. .498
/organism="Mus musculus"
/strain=C57BL/6J"
/db_xref="taxon:10090"
/clone="RPCI-23-258K23"
/clone_lib="RPCI-23"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2405 CTGACCTTAAAGACATCCTGAGCGAGG 2431
                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
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Best Local Similarity
Matches 419; Conserv
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